

RECEIVED  
 JUN 12 2001  
 TECH CENTER 1600, 2900

SEQUENCE LISTING

<110> UNIVERSITY, Illinois U.

<120> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS

<130> 1610-107F

<140> 19-490,361

<141> 2000-11-27

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 1335

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2335)

<230>

<231> CDS

<232> (83)..(2173)

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 Met Ala Glu Ala Pro Pro Arg Arg Leu Gly  
 1 5 10

ctc ggt ccc ccg ccc ggg gac gcc ccc cgc ggc gag cta gtg ggc ctc 160  
 Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu  
 15 20 25

acc gcc gtg cag agc gaa cag gcc gag gcc gcc ggg gcc gcc tcc ccg 208  
 Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro  
 30 35 40

cgc cgc ctc gcc ctc ctg gcc agc ccc ctg ccg ccg gcc gcc ccc ctc 256  
 Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu  
 45 50 55

cct ggg ccg gcc tcc gcc tgg gcc tcc gcc tgc gcc cag cgc tcc tgg 304  
 Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser  
 60 65 70

gcc gcc cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg 352  
 Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val  
 75 80 85 90

ctc gag cgg ccc cgc gcc tgg gcc ttc gtc tac cag gtc ttc ata ttt 400



Leu	Ala	Arg	Ile	Arg	Gly	Ile	Ala	Ile	Val	Tyr	His	Val	Ile	Ile	Ile	
atg	atg	gtg	ttc	aac	tgc	ctg	gta	gta	tat	gtg	gtg	ttc	aac	atg	atg	448
Leu	Leu	Val	Phe	Ser	Cys	Leu	Val	Leu	Ser	Val	Leu	Ser	Thr	Ile	Gln	
			111						113				111			
gag	gac	gag	gaa	gtt	gac	aac	gag	tgt	gtc	gtc	atc	ttg	gaa	ttc	gtg	496
Gln	His	Gln	Gln	Leu	Ala	Asn	Gln	Cys	Leu	Leu	Ile	Leu	Gln	Phe	Val	
			126				137					133				
atg	atc	gtg	gtt	ttc	ggc	ttg	gag	tac	atc	gtc	agg	gtc	ttg	ttc	gtc	544
Met	Ile	Val	Val	Phe	Gly	Leu	Gln	Tyr	Ile	Val	Arg	Val	Trp	Ser	Ala	
	140				143						150					
gga	tgc	tgc	tgc	ggc	tac	gga	gga	tgg	cag	ggc	ggc	ttc	ggc	ttt	ggc	592
Gly	Cys	Cys	Cys	Arg	Tyr	Arg	Gly	Trp	Gln	Gly	Arg	Phe	Arg	Phe	Ala	
155				160						165					170	
aga	aag	ccc	ttc	tgt	gtc	atc	gac	ttc	atc	gtg	ttc	gtg	ggc	tgc	gtg	640
Arg	Lys	Pro	Phe	Cys	Val	Ile	Asp	Phe	Ile	Val	Phe	Val	Ala	Ser	Val	
				175					180					185		
ggc	gtc	atc	ggc	ggc	ggc	acc	cag	ggc	aac	atc	ttc	ggc	acg	ttc	ggc	688
Ala	Val	Ile	Ala	Ala	Gly	Thr	Gln	Gly	Asn	Ile	Phe	Ala	Thr	Ser	Ala	
			190					195					200			
ctg	ggc	agg	atg	ggc	ttc	ctg	cag	atc	ctg	ggc	atg	gtg	ggc	atg	gac	736
Leu	Arg	Ser	Met	Arg	Phe	Leu	Gln	Ile	Leu	Arg	Met	Val	Arg	Met	Asp	
			205				210					215				
ggc	ggc	ggc	ggc	acc	tgg	aag	ctg	ctg	ggc	tca	gtg	gtc	tac	ggc	cat	784
Arg	Arg	Gly	Gly	Thr	Trp	Lys	Leu	Leu	Gly	Ser	Val	Val	Tyr	Ala	His	
	220				225					230						
agg	aag	gag	ctg	atc	acc	ggc	tgg	tac	atc	ggg	ttc	ctg	gtg	ttc	atc	832
Ser	Cys	Gln	Leu	Ile	Thr	Ala	Trp	Tyr	Ile	Gly	Phe	Leu	Val	Leu	Ile	
235				240					245					250		
ttc	ggc	ttc	ttc	ctg	gtc	tac	ctg	ggc	gag	aag	gac	ggc	aac	ttc	gac	880
Phe	Ala	Ser	Phe	Leu	Val	Tyr	Leu	Ala	Glu	Lys	Asp	Ala	Asn	Ser	Asp	
				255				260					265			
ttc	ttc	ttc	tac	ggc	gac	tgc	ctc	tgg	tgg	ggg	acg	att	aca	ttg	aca	928
Phe	Ser	Ser	Tyr	Ala	Asp	Ser	Leu	Trp	Trp	Gly	Thr	Ile	Thr	Leu	Thr	
			270					275				280				
acc	atc	ggc	tac	ggc	gac	aag	aca	ccg	cac	aca	tgg	ctg	ggc	agg	gtc	976
Thr	Ile	Gly	Tyr	Gly	Asp	Lys	Thr	Pro	His	Thr	Trp	Leu	Gly	Arg	Val	
		285					290				295					
ctg	gct	gct	ggc	ttc	ggc	tta	ctg	ggc	atc	tct	ttc	ttt	ggc	ctg	gct	1024
Leu	Ala	Ala	Gly	Phe	Ala	Leu	Leu	Gly	Ile	Ser	Phe	Phe	Ala	Leu	Pro	
	300					305					310					
ggc	ggc	atc	cta	ggc	ttc	ggc	ttt	ggc	ctg	aag	gtc	cag	gag	cag	cac	1072
Ala	Gly	Ile	Leu	Gly	Ser	Gly	Phe	Ala	Leu	Lys	Val	Gln	Glu	Gln	His	

[illegible]

1881  
 Phe Lys Asp Val Lys Asp Val Ile Ala Gln Tyr Ser Ala Gly His Leu  
 601 605 610

1884  
 Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile  
 608 612 616

1887  
 Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Gln Lys Gly Asp Lys  
 619 623 627

1886  
 Gly Pro Ser Asp Ala Gln Val Val Asp Gln Ile Ser Met Met Gly Arg  
 625 630 635

1884  
 Val Val Lys Val Gln Lys Gln Val Gln Ser Ile Gln His Lys Leu Asp  
 620 625 630

2032  
 Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala  
 635 640 645 650

2080  
 Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser  
 655 660 665

2128  
 Asp Tyr His Ser Pro Val Asp His Glu Asp Ile Ser Val Ser Ala Gln  
 670 675 680

2170  
 Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp  
 685 690 695

2230  
 gggaattctc agaggcaggg cagcacacgg ccagccccgc ggactggcgc tccgactgcc

2290  
 ctctagggc tccggactcc tctcgtaatt gaactcactc cctcacgggg agagagacca

2335  
 caagagatat tgagctgact gactggggcgt ggtacctgct gtggg

2210: 2  
 2211: 695  
 2212: PRT  
 2213: Homo sapiens

2400: 2  
 Met Ala Glu Ala Pro Pro Arg Arg Leu Gly Leu Gly Pro Pro Pro Gly  
 1 5 10 15  
 Asp Ala Pro Arg Ala Glu Leu Val Ala Leu Thr Ala Val Gln Ser Glu  
 20 25 30  
 Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu  
 35 40 45  
 Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly

Ser Gly Ser Ala Tyr Gly His Asn Ser Ser Ala Ala His Lys Asn Tyr  
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 Arg Arg Leu Gln Asn Trp Val Tyr Asn Val Leu Gln Arg Phe Arg Gly  
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 Trp Ala Phe Val Tyr His Val Phe Ile Phe Leu Leu Val Phe Ser Cys  
 120  
 Leu Val Leu Ser Val Leu Ser Thr Ile Gln Gln His Gln Gln Leu Ala  
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 Asn Gln Cys Leu Leu Ile Leu Gln Phe Val Met Ile Val Val Phe Gly  
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 Leu Gln Tyr Ile Val Arg Val Trp Ser Ala Gly Cys Cys Cys Arg Tyr  
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 Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala Arg Lys Pro Phe Cys Val  
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 Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly  
 170  
 Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe  
 180  
 Leu Gln Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp  
 190  
 Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Gln Leu Ile Thr  
 200  
 Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val  
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 Tyr Leu Ala Gln Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp  
 220  
 Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp  
 230  
 Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala  
 240  
 Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser  
 250  
 Gly Phe Ala Leu Lys Val Gln Gln Gln His Arg Gln Lys His Phe Gln  
 260  
 Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu  
 270  
 Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr  
 280  
 Tyr Asp Ser Ile Leu Pro Ser Phe Arg Gln Leu Ala Leu Leu Phe Glu  
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 His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Gln Val Arg  
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 Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala  
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 Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Gln Ser Ser  
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 Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg  
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 Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser  
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 Pro Ser Ser Gln Gln Val Gly Gln Ala Thr Ser Pro Thr Lys Val Gln  
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 Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg  
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 Leu Lys Pro Arg Thr Ser Ala Gln Asp Ala Pro Ser Gln Gln Val Ala  
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<210> 4

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<212> DNA

<213> Artificial Sequence

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<221> Description of Artificial Sequence: PCR Primer

<400> 4

aggcaggt tgccgggga aacg

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<210> 5

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

\*C100 - Description of Artificial Sequence: PCR Primer

\*C101 - 6

agagagagag agagagag agg

\*C210 - 6

\*C211 - 21

\*C212 - DNA

\*C213 - Artificial Sequence

\*C221 -

\*C223 - Description of Artificial Sequence: PCR Primer

\*C401 - 6

agagagagag agagagag g

21

\*C210 - 7

\*C211 - 20

\*C212 - DNA

\*C213 - Artificial Sequence

\*C221 -

\*C223 - Description of Artificial Sequence: PCR Primer

\*C401 - 7

agagagagag agagagag

20

\*C101 - 8

\*C111 - 20

\*C112 - DNA

\*C113 - Artificial Sequence

\*C221 -

\*C223 - Description of Artificial Sequence: PCR Primer

\*C401 - 8

agagagagag agagagag

20

\*C101 - 9

\*C111 - 21

\*C112 - DNA

\*C113 - Artificial Sequence

\*C221 -

\*C223 - Description of Artificial Sequence: PCR Primer

\*C401 - 9

agagagagag agagagag a

21

\*C101 - 10

\*C111 - 21

\*C112 - DNA

<410> Artificial Sequence

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<410> 11

<411> 21

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<413> Artificial Sequence

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<420> Description of Artificial Sequence: PCR Primer

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<410> 12

<411> 21

<412> DNA

<413> Artificial Sequence

<420>

<420> Description of Artificial Sequence: PCR Primer

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<410> 13

<411> 21

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<413> Artificial Sequence

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<410> 14

<411> 19

<412> DNA

<413> Artificial Sequence

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<210> Description of Artificial Sequence: PCR Primer

<400> 14

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<210> 15

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<212> DNA

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: PCR Primer

<400> 15

gatagcnaag agatggagag g

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<210> 16

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<212> DNA

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<213> Description of Artificial Sequence: PCR Primer

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aattcaactg cagcagtgag c

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<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: PCR Primer

<400> 17

gtgcttctc ctccatcagg c

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<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: PCR Primer

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aacgatact ccccatgtca

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<210> 19

<211> 20

<212> DNA

<110> Artificial Sequence

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<112> Description of Artificial Sequence: PCR Primer

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23

<110> 21

<111> 24

<112> DNA

<113> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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gttgaggaggag tgagttcaag taag

24

<110> 31

<111> 24

<112> DNA

<113> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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actacatgat ggagggccct ctgc

24

<110> 32

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<112> DNA

<113> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

<400> 32

tcacacacgc taagctcaca ctgg

24

<110> 33

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<112> PRT

<113> Homo sapiens

<400> 33

Met Ala Ala Ala Ser Ser Pro Pro Arg Ala Glu Arg Lys Arg Trp Gly  
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Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys  
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Tyr Tyr Ile Ile Ser Leu Ala Leu Ala Gly Gly Ile Ala Gly Gly  
 40 45  
 Ala Leu Tyr Ala Ile Ile Ala Phe Gly Ala Phe Gly Phe Ala Phe Phe  
 50 55  
 Ala Ser Phe Ala Ala Phe Ala Ala Phe Phe Val Ala Ser Asp Leu Gly  
 60 65  
 Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr  
 70 75  
 Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn  
 80 85  
 Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala  
 90 95  
 Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr  
 100 105  
 Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu  
 110 115  
 Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp  
 120 125  
 Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg  
 130 135  
 Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala  
 140 145  
 Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr  
 150 155  
 Ser Ala Ile Arg Gly Ile Arg Phe Leu Gln Ile Leu Arg Met Leu His  
 160 165  
 Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe  
 170 175  
 Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly  
 180 185  
 Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val  
 190 195  
 Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp  
 200 205  
 Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val Pro  
 210 215  
 Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala  
 220 225

140 Ser His His Ala Leu His Ala Lys Leu Leu Lys Ser Gly His Ala  
 341 346 347  
 150 Lys Val His His Lys His Arg His Lys His His Asn Arg His His  
 351 357 361  
 160 Pro Ala Ala Ala Ser Leu Ile His Thr Ala Trp Arg Lys Tyr Ala Ala  
 371 378 381  
 170 Gln Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro  
 385 391 395 401  
 180 Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val  
 405 411 418  
 190 Val Val Lys Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr  
 420 425 430  
 200 Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro  
 435 440 445  
 210 Glu Gln Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser  
 450 455 460  
 220 Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met  
 465 470 475 480  
 230 Arg Thr Asn Ser Phe Ala Glu Asp Leu Asp Leu Glu Gly Glu Thr Leu  
 485 490 495  
 240 Leu Thr Pro Ile Thr His Ile Ser Gln Leu Arg Glu His His Arg Ala  
 500 505 510  
 250 Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys Lys  
 515 520 525  
 260 Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Glu Gln  
 530 535 540  
 270 Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln  
 545 550 555 560  
 280 Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val  
 565 570 575  
 290 Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu  
 580 585 590  
 300 Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu  
 595 600 605  
 310 Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr  
 610 615 620  
 320 Pro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr Gln  
 625 630 635 640

11 Tyr Arg Ser Gly Arg Ser Val Arg Ile Ala Leu Ile Ile Ile Ser  
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Asn Thr Leu Pro Thr Tyr Ala Ala Leu Thr Val Ile Arg Arg Gly Pro  
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Asp Glu Gly Ser  
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<211> 34  
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<211> PRT  
<213> Homo sapiens

<400> 34  
Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly  
1 5 10 15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro  
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro  
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala  
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe  
65 70 75 81

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His  
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe  
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile  
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg  
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg  
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu  
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe  
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met  
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val  
210 215 220

Val Tyr Ala His Ser Lys Ala Ser Val Thr Ala Tyr Tyr Ile Lys His  
 225 230 235 240 245 250 255 260 265 270 275 280 285 290

Leu Lys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly  
 295 300 305 310 315 320 325 330 335 340 345 350 355 360

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu  
 365 370 375 380 385 390 395 400 405 410 415 420 425 430

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp  
 435 440 445 450 455 460 465 470 475 480 485 490 495 500

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe  
 505 510 515 520 525 530 535 540 545 550 555 560 565 570

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val  
 575 580 585 590 595 600 605 610 615 620 625 630 635 640

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala  
 645 650 655 660 665 670 675 680 685 690 695 700 705 710

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser  
 715 720 725 730 735 740 745 750 755 760 765 770 775 780

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr  
 785 790 795 800 805 810 815 820 825 830 835 840 845 850

Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu  
 855 860 865 870 875 880 885 890 895 900 905 910 915 920

Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro  
 925 930 935 940 945 950 955 960 965 970 975 980 985 990

Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe  
 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060

Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala  
 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130

Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser  
 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200

Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala  
 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270

Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu  
 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340

Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro  
 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410

Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile  
 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480

Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys  
 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550



Val	Asp	Leu	Asp	Pro	Tyr	Arg	Val	Met	Asp	Val	Ile	Glu	Gln	Pro	Asp	
148					151					154						
Ala	Gly	His	Leu	Asp	Met	Leu	Ser	Arg	Ile	Lys	Ser	Leu	Gln	Ser	Arg	
149				151						151					150	
Val	Asp	Gln	Ile	Val	Gly	Arg	Gly	Pro	Ala	Ile	Thr	Asp	Lys	Asp	Arg	
				160					171					170		
Thr	Lys	Gly	Pro	Ala	Glu	Ala	Glu	Leu	Pro	Glu	Asp	Pro	Ser	Met	Met	
			181					183					184			
Gly	Arg	Leu	Gly	Lys	Val	Glu	Lys	Gln	Val	Leu	Ser	Met	Glu	Lys	Lys	
	194					190					198					
Leu	Asp	Phe	Leu	Val	Asn	Ile	Tyr	Met	Gln	Arg	Met	Gly	Ile	Pro	Pro	
610					613						620					
Thr	Glu	Thr	Glu	Ala	Tyr	Phe	Gly	Ala	Lys	Glu	Pro	Glu	Pro	Ala	Pro	
625					630					635					640	
Pro	Tyr	His	Ser	Pro	Glu	Asp	Ser	Arg	Glu	His	Val	Asp	Arg	His	Gly	
				645					650					655		
Cys	Ile	Val	Lys	Ile	Val	Arg	Ser	Ser	Ser	Ser	Thr	Gly	Gln	Lys	Asn	
			660					665					670			
Phe	Ser	Ala	Pro	Pro	Ala	Ala	Pro	Pro	Val	Gln	Cys	Pro	Pro	Ser	Thr	
			675				681					685				
Ser	Trp	Gln	Pro	Gln	Ser	His	Pro	Arg	Gln	Gly	His	Gly	Thr	Ser	Pro	
690						695					700					
Val	Gly	Asp	His	Gly	Ser	Leu	Val	Arg	Ile	Pro	Pro	Pro	Pro	Ala	His	
705					710					715					720	
Glu	Arg	Ser	Leu	Ser	Ala	Tyr	Gly	Gly	Gly	Asn	Arg	Ala	Ser	Met	Glu	
				725					730					735		
Phe	Leu	Arg	Gln	Glu	Asp	Thr	Pro	Gly	Cys	Arg	Pro	Pro	Glu	Gly	Thr	
			741					745					750			
Leu	Arg	Asp	Ser	Asp	Thr	Ser	Ile	Ser	Ile	Pro	Ser	Val	Asp	His	Glu	
			755				761					765				
Glu	Leu	Glu	Arg	Ser	Phe	Ser	Gly	Phe	Ser	Ile	Ser	Gln	Ser	Lys	Glu	
770						775					780					
Asn	Leu	Asp	Ala	Leu	Asn	Ser	Cys	Tyr	Ala	Ala	Val	Ala	Pro	Cys	Ala	
785					790					795					800	
Lys	Val	Arg	Pro	Tyr	Ile	Ala	Glu	Gly	Glu	Ser	Asp	Thr	Asp	Ser	Asp	
				805					810					815		
Leu	Cys	Thr	Pro	Cys	Gly	Pro	Pro	Pro	Arg	Ser	Ala	Thr	Gly	Glu	Gly	
			820					825					830			

Met Gly Asp Val Gly Trp Ala Gly Phe Arg Lys  
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<411> 37

<411> 401

<411> 437

<411> Hum. sapiens

<411> 38

Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly  
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Asp Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp  
20 25 30

Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly  
35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp  
50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg  
65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro  
85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr  
100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu  
115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr  
130 135 140

Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Leu Glu  
145 150 155 160

Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile Trp  
165 170 175

Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys  
180 185 190

Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala  
195 200 205

Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr  
210 215 220

Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met  
225 230 235 240

Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala

His Ser Lys Ala Leu Ile Thr Ala Tyr Tyr Ile Gly Ile Leu Thr Leu  
 275 280 285  
 Ile Leu Ser Ser Ile Leu Val Tyr Leu Val Ala Lys Asp Val Pro Glu  
 290 295 300  
 Val Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr Ala  
 305 310 315 320  
 Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly  
 325 330 335 340  
 Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe  
 345 350 355 360  
 Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly  
 365 370 375 380  
 Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe  
 385 390 395 400  
 Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp Arg  
 405 410 415 420  
 Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg  
 425 430 435 440  
 Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln Leu  
 445 450 455 460  
 Glu Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg Leu  
 465 470 475 480  
 Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu  
 485 490 495 500  
 Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val  
 505 510 515 520  
 Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala  
 525 530 535 540  
 Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met  
 545 550 555 560  
 Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile  
 565 570 575 580  
 Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg  
 585 590 595 600  
 Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys  
 605 610 615 620  
 Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg

Ile Lys Tyr Leu Val Thr Arg Ile Asp Met Ile Thr Thr Leu Gly Ile  
 605 610

Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr  
 615 620

Phe Pro Ser Gln Gln Ser Pro Arg Asn Gln Pro Tyr Val Ala Arg Pro  
 625 630

Ser Thr Ser Gln Ile Gln Asp Gln Ser Met Met Gly Lys Phe Val Lys  
 635 640

Val Gln Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val  
 645 650

Asp Met His Met Gln His Met Gln Arg Leu Gln Val Gln Val Thr Gln  
 655 660

Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Gln Ala Gln Lys Lys  
 665 670

Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asn Tyr Ser  
 675 680

Glu Thr Gly Pro Pro Gln Pro Pro Tyr Ser Phe His Gln Val Thr Ile  
 685 690

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu  
 695 700

Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser  
 705 710

Ser Ala Thr Thr Tyr Val Gln Arg Pro Thr Val Leu Pro Ile Leu Thr  
 715 720

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly  
 725 730

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg  
 735 740

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu  
 745 750

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr  
 755 760

Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr  
 765 770

Leu Ala Gln Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser  
 775 780

Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val  
 785 790



<119> Artificial Sequence

<120>

<121> Description of Artificial Sequence: PCR Primer

<419> 41

caaaatattg aacatattgt agc

24

<211> 41

<212> 24

<213> DNA

<214> Artificial Sequence

<220>

<221> Description of Artificial Sequence: PCR Primer

<400> 41

cagaagagtc aagatgggca ggac

24